Table S1. Detected mutations in the viruses from the survivor and the new EVD cluster

Branch no.	EBOV gene	Nucleotide position	Nucleotide change	Amino acid position	Amino acid change
1	NP	898	T→C	–	–
1	IGR	4364	T→A	–	–
1	L	4593	T→C	–	–
1	IGR	18339	T→C	–	–
2	IGR	256	A→G	–	–
2	GP	78	T→C	–	–
2	VP30	845	G→A	282	W→Stop (truncation by 7 residues)
2	IGR	9764	T→C	–	–
2	IGR	18408	A→G	–	–
3	NP	20	A→G	7	K→R

NP, nucleoprotein; GP, glycoprotein; L; large (polymerase); IGR, intergenic region.

Branch numbers refers to the annotations given in Figure 1B: 1, signature of single nucleotide polymorphisms specific for the virus in the acute sample of the survivor (EM_076610, accession KR817153); 2, differences between the survivor's acute sample from 2014 (EM_076610, accession KR817153) and his seminal fluid sample from 2016 (note that the signature of branch 2 is also found in the viruses from cases 4, 5, and 7); 3, differences between the seminal fluid sample and the acute samples of cases 6, 8, and 9. Where a gene is given the numbering is from the first nucleotide or amino acid in the coding sequence. Mutations in intergenic regions are given coordinates from the first nucleotide in EM_076610 (accession KR817153).